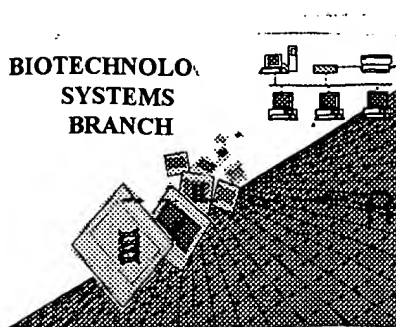


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/613 092

Source: 1653

Date Processed by STIC: 11/29/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/613,092

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 J Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1653

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/613,092 DATE: 11/29/2000
 TIME: 08:54:57

Input Set : A:\68430Seq.txt
 Output Set: N:\CRF3\11292000\1613092.raw

Does Not Comply
 Corrected Diskette Needed

ppr 1-2

Suggestion:

Consult

Sequence Rules

4 <110> APPLICANT: ADES, EDWIN W.
 5 SAMPSON, JACQUELYN S.
 6 THARPE, JEAN A.
 7 JOHNSON, SCOTT E.
 8 JUE, DANNY L.
 9 CARLONE, GEORGE M.
 10 ZEILER, JOAN L.
 11 WESTERLINK, MARIA ANNA J.
 13 <120> TITLE OF INVENTION: Multiple Antigenic Peptides Immunogenic Against
 14 STREPTOCOCCUS PNEUMONIAE
 16 <130> FILE REFERENCE: 68430 US
 18 <140> CURRENT APPLICATION NUMBER: US/09/613,092
 19 <141> CURRENT FILING DATE: 2000-07-10
 21 <150> PRIOR APPLICATION NUMBER: US 07/791,377
 22 <151> PRIOR FILING DATE: 1991-09-17
 24 <150> PRIOR APPLICATION NUMBER: US 07/816,286
 25 <151> PRIOR FILING DATE: 1992-01-03
 27 <150> PRIOR APPLICATION NUMBER: US 08/222,179
 28 <151> PRIOR FILING DATE: 1994-04-04
 30 <150> PRIOR APPLICATION NUMBER: US 08/715,131
 31 <151> PRIOR FILING DATE: 1996-09-17
 33 <150> PRIOR APPLICATION NUMBER: US 09/221,753
 34 <151> PRIOR FILING DATE: 1998-12-28
 36 <150> PRIOR APPLICATION NUMBER: US 60/076,565
 37 <151> PRIOR FILING DATE: 1998-03-02
 39 <150> PRIOR APPLICATION NUMBER: PCT US/99/04326
 40 <151> PRIOR FILING DATE: 1999-2-26
 42 <160> NUMBER OF SEQ ID NOS: 10
 44 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

213 <210> SEQ ID NO: 5
 214 <211> LENGTH: 15
 E--> 215 <212> TYPE: amino acid
 216 <213> ORGANISM: UNKNOWN
 218 <220> FEATURE:
 219 <223> OTHER INFORMATION: PEPTIDE
 221 <400> SEQUENCE: 5
 222 Thr Val Ser Arg Val Pro Trp Thr Ala Trp Ala Phe His Gly Tyr
 223 1 5 5 10 10 10 15
 225 <210> SEQ ID NO: 6
 226 <211> LENGTH: 15
 E--> 227 <212> TYPE: amino acid
 228 <213> ORGANISM: UNKNOWN
 230 <220> FEATURE:

use PRT, when in new sequence rules format
 invalid response - give source of genetic material

15 1
 delete

(see
 circled
 portion of
 item 12 on
 Even Summary
 sheet)

misaligned
 amino acid
 nos. Per
 Sequence Rules,
 number the amino
 acids under every 5
 amino acids

RAW SEQUENCE LISTING DATE: 11/29/2000
 PATENT APPLICATION: US/09/613,092 TIME: 08:54:57

Input Set : A:\68430Seq.txt
 Output Set: N:\CRF3\11292000\I613092.raw

```

231 <223> OTHER INFORMATION: PEPTIDE
233 <400> SEQUENCE: 6
234 Arg Ser Tyr Gln His Asp Leu Arg Ala Tyr Gly Phe Trp Arg Leu
235      5              10              15
237 <210> SEQ ID NO: 7
238 <211> LENGTH: 15
E--> 239 <212> TYPE: amino acid
240 <213> ORGANISM: UNKNOWN
242 <220> FEATURE:
243 <223> OTHER INFORMATION: PEPTIDE
245 <400> SEQUENCE: 7
246 Leu Val Arg Arg Phe Val His Arg Arg Pro His Val Glu Ser Gln
247      5              10              15
249 <210> SEQ ID NO: 8
250 <211> LENGTH: 15
E--> 251 <212> TYPE: amino acid
252 <213> ORGANISM: UNKNOWN
254 <220> FEATURE:
255 <223> OTHER INFORMATION: PEPTIDE
257 <400> SEQUENCE: 8
258 Leu Val Arg Arg Phe Val His His Arg Pro His Val Glu Ser Gln
259      5              10              15
261 <210> SEQ ID NO: 9
262 <211> LENGTH: 15
E--> 263 <212> TYPE: amino acid
264 <213> ORGANISM: UNKNOWN
266 <220> FEATURE:
267 <223> OTHER INFORMATION: PEPTIDE
269 <400> SEQUENCE: 9
270 Leu Val Arg Arg Phe Val His Arg Pro His Val Glu Ser Gln Lys
271      5              10              15
W--> 272 <210> SEQ ID NO: 10
273 <211> LENGTH: 15
E--> 274 <212> TYPE: amino acid
275 <213> ORGANISM: UNKNOWN
277 <220> FEATURE:
278 <223> OTHER INFORMATION: PEPTIDE
280 <400> SEQUENCE: 10
281 Ser Tyr Gln His Asp Leu Arg Ala Tyr Gly Phe Trp Arg Leu Lys
282      1              5              10              15

```

OK

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/613,092

DATE: 11/29/2000

TIME: 08:54:58

Input Set : A:\68430Seq.txt

Output Set: N:\CRF3\11292000\I613092.raw

RECEIVED

DEC 13 2000

TECH CENTER 1600/2900

L:18 M:270 C: Current Application Number differs, Replaced Application Number
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:215 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:227 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:239 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:251 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:263 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:272 M:283 W: Missing Blank Line separator, <210> field identifier
L:274 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: